1642

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/509,779*

DATE: 02/01/2001
TIME: 21:16:57

INPUT SET: S36345.raw

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FEB 0 5 ~~

TECH CENTER 1600 ~~~

<table>
<tr><td colspan="2">

This Raw Listing contains the General
Information Section and up to the first 5 pages.
</td></tr>
</table>

```
 1                               SEQUENCE LISTING
 2
 3      (1)     General Information:
 4                                                          Does Not Comply
 5          (i)  APPLICANT:        ↑ move up – all responses   Corrected Diskette Needed
 6              (A) NAME: Yi Sun                must be on
 7              (B) STREET: 4841 Hillway Court         same line as heading
 8              (C) CITY: Ann Arbor
 9              (D) STATE: Michigan
10              (E) COUNTRY: USA
11     delete  (F) POSTAL CODE (ZIP): 48105                     insert these
12              (G) TELEPHONE: (313) 996-1959                  MANDATORY
13              (H) TELEFAX: (313) 996-7158                    headings and
14                                                              their
15          (ii) TITLE OF INVENTION: Sensitive to Apoptosis Gene (SAG)  responses
16                                                                       for a U.S.
17          (iii) NUMBER OF SEQUENCES: 50      →    (iv) CORRESPONDENCE ADDRESS:   case
18                                                        (A) ADDRESSEE:
19     (v)  (iv) COMPUTER READABLE FORM:                 (B) STREET:
20              (A) MEDIUM TYPE: Floppy disk             (C) CITY:
21              (B) COMPUTER: IBM PC compatible          (D) STATE:
22              (C) OPERATING SYSTEM: PC-DOS/MS-DOS      (E) COUNTRY:
23              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)   (F) ZIP:
24     (v) CURRENT APPLICATION DATA:  ←    insert these mandatory headings
25         (A) APPLICATION NUMBER:
           (B) FILING DATE:
26      (2) INFORMATION FOR SEQ ID NO: 1:
27
28          (i) SEQUENCE CHARACTERISTICS:
29              (A) LENGTH: 1140 base pairs
30              (B) TYPE: nucleic acid
31              (C) STRANDEDNESS: double       FYI: EPO format
32              (D) TOPOLOGY: linear               is invalid
33                                             for U.S. cases
34          (ii) MOLECULE TYPE: cDNA
35
36
37          (ix) FEATURE:
38              (A) NAME/KEY: CDS
39              (B) LOCATION:17..355
40
41          (ix) FEATURE:
42              (A) NAME/KEY: mat_peptide
43              (B) LOCATION:17..355
44
45          (ix) FEATURE:
46              (A) NAME/KEY: misc_feature
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47              (B) LOCATION:1..1140
48              (D) OTHER INFORMATION:/note= "Mouse SAG"
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51      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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54                     Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys
55                      1               5                   10
56
57      GTC CTT TCT TCG CAC TCC GGG AGC GCA GGC TCC AAG TCG GGA GGC GAC     97
58      Val Leu Ser Ser His Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp
59               15                  20                  25
60
61      AAG ATG TTC TCT CTC AAG AAG TGG AAC GCG GTA GCC ATG TGG AGC TGG    145
62      Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp
63               30                  35                  40
64      GAC GTT GAG TGC GAT ACC TGT GCC ATC TGC AGG GTC CAG GTG ATG GAT    193
65      Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp
66           45                  50                  55
67
68      GCC TGC CTT CGA TGT CAA GCT GAA AAC AAG CAA GAG GAC TGT GTT GTG    241
69      Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val
70       60                  65                  70                  75
71
72      GTC TGG GGA GAG TGT AAC CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG    289
73      Val Trp Gly Glu Cys Asn His Ser Phe His Asn Cys Cys Met Ser Leu
74                   80                  85                  90
75
76      TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC CAG CAG GAC TGG GTA    337
77      Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val
78               95                  100                 105
79
80      GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCGCT CCTGGTGTGG           385
81      Val Gln Arg Ile Gly Lys
82               110
83
84      TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTC ATCCTTGAGA GAGAGAGGAT   445
85
86      GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTTATTA ATTTGTCTGT TTAGTTTTGG   505
87
88      GAAATTCTCT ACAATTAAGA TAATTTGTTA AAAATGGCCT TTCCTACCTC TGGTGTGTGT   565
89
90      GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA TGATCTTTGT TTATCTGTAC   625
91
92      CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTTG TGTTTATGCT TGAGGGTTAA   685
93
94      AAAATAGATA AACGAATGTT ACAGTAACAA ATAAAATGCA TTGAAAAGCC GACTCCTCCT   745
95
96      AATCCTTTTT GTGTTGGGAG AGAGGCAAGC GAGGCCACCC TGCTGTCTTC ATTTGCTGTG   805
97
98      AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCGTAACT GTCGGGTAAA CTGTAATATG   865
99
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INPUT SET: S36345.raw

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100    GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC CATCTTTGAC TTGGCCAGGA    925
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102    AGCCTGGATT GTTCAACCAC TTAGTTCTAA AGAACTGTTT TCTGTTTTTG CCGAAGGTTG    985
103
104    TATTGTATGT TTTAGTCAAA AATATTAGTA GGAAAATGGC TTACTAGTAT AACACTGAAG    1045
105
106    TTCATTATGC AATGTTTTAA TAAAATATTG TGCTTTGAGT TATTAAAGTT TGATATATAC    1105
107
108    TCTTAAAATC ATTAAACTAA TTCATCAATT AAATG                              1140
109
110
111    (2) INFORMATION FOR SEQ ID NO: 2:
112
113         (i) SEQUENCE CHARACTERISTICS:
114            (A) LENGTH: 113 amino acids
115            (B) TYPE: amino acid
116            (D) TOPOLOGY: linear
117
118         (ii) MOLECULE TYPE: protein
119         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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121    Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys Val Leu Ser Ser His
122     1               5                  10                  15
123
124    Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
125                20                  25                  30
126
127    Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
128            35                  40                  45
129
130    Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
131        50                  55                  60
132
133    Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
134     65                  70                  75                  80
135
136    Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
137                85                  90                  95
138
139    Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
140                100                 105                 110
141
142    Lys
143
144
145    (2) INFORMATION FOR SEQ ID NO: 3:
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147         (i) SEQUENCE CHARACTERISTICS:
148            (A) LENGTH: 754 base pairs
149            (B) TYPE: nucleic acid
150            (C) STRANDEDNESS: double
151            (D) TOPOLOGY: linear
152
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153        (ii)  MOLECULE TYPE: cDNA
154
155
156        (ix)  FEATURE:
157               (A)  NAME/KEY: CDS
158               (B)  LOCATION:1..339
159
160        (ix)  FEATURE:
161               (A)  NAME/KEY: mat_peptide
162               (B)  LOCATION:1..339
163
164        (ix)  FEATURE:
165               (A) ·NAME/KEY: misc_feature
166               (B)  LOCATION:1..754
167               (D)  OTHER INFORMATION:/note= "Human SAG"
168
169
170        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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172 ·  ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC        48
173    Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
174     1               5                  10                  15
175
176    TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC        96
177    Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
178               20                  25                  30
179
180    AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT       144
181    Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
182           35                  40                  45
183
184    ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT       192
185    Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
186        50                  55                  60 ·
187
188    CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT       240
189    Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
190    65                  70                  75                  80
191
192    AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC       288
193    Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
194                    85                  90 ·                95
195
196    AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC       336
197    Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
198                    100                 105                 110
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200    AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA            389
201    Lys
202
203
204    TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG      449
205
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INPUT SET: S36345.raw

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206    GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT    509
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208    ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC    569
209
210    TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT    629
211
212    GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT    689
213
214    TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT    749
215
216    TTAAA                                                                754
217
218
219    (2) INFORMATION FOR SEQ ID NO: 4:
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221            (i) SEQUENCE CHARACTERISTICS:
222                (A) LENGTH: 113 amino acids
223                (B) TYPE: amino acid
224                (D) TOPOLOGY: linear
225
226        (ii) MOLECULE TYPE: protein
227        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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229    Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
230     1               5                  10                  15
231
232    Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
233             20                  25                  30
234
235    Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
236             35                  40                  45
237
238    Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
239         50                  55                  60
240
241    Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
242     65                  70                  75                  80
243
244    Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
245                 85                  90                  95
246
247    Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
248             100                 105                 110
249
250    Lys
251
252
253    (2) INFORMATION FOR SEQ ID NO: 5:
254
255            (i) SEQUENCE CHARACTERISTICS:
256                (A) LENGTH: 18 base pairs
257                (B) TYPE: nucleic acid
258                (C) STRANDEDNESS: single
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/509,779*

INPUT SET: S36345.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Yi Sun
7	Unknown or Misplaced Identifier	(B) STREET: 4841 Hillway Court
8	Unknown or Misplaced Identifier	(C) CITY: Ann Arbor
9	Unknown or Misplaced Identifier	(D) STATE: Michigan
10	Unknown or Misplaced Identifier	(E) COUNTRY: USA
11	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 48105
12	Unknown or Misplaced Identifier	(G) TELEPHONE: (313) 996-1959
13	Unknown or Misplaced Identifier	(H) TELEFAX: (313) 996-7158

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/09/509,779*

INPUT SET: S36345.raw

ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA